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SEQUENCE LISTING

<110> COR Therapeutics, Inc.
Ramakrishnan, Vanitha
Phillips, David

<120> Transgenic Animals Having a Modified Glycoprotein V
Gene and Methods for Their Use

<130> 44481-5044-WO

<140> PCT/US99/17594

<141> 1999-08-04

<150> US 60/109,797

<151> 1998-08-04

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<220>

<221> variation

<222> (13)..(18)

<223> y at position 13 = c or t; r at position 18 = a or
g.

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<213> Homo sapiens

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0975803-02001

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<213> Artificial Sequence

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<221> variation
<222> (3)..(21)
<223> y at position 3 = c or t; r at positions 6 and 21
= a or g.

<400> 3
gayaaratgg tgytcytgga rca

23

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<212> PRT
<213> Homo sapiens

<220>
<223> Amino acid sequence corresponding to primer of
seq. id no. 7.

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Asp Lys Met Val Leu Leu Glu Gln
1 5

<210> 5
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

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<221> variation
<222> (3)..(24)
<223> y at positions 3, 12, 15, 18 and 19 = c or t; v at
position 6 = a or c or g; m at position 9 = a or
c; s at position 24 = c or g.

<400> 5
ccyggvacmt tyagygayyt gatsaa

26

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<211> 9
<212> PRT
<213> Homo sapiens

<400> 6
Pro Gly Thr Phe Ser Asp Leu Ile Lys

<210> 7
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

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 <221> variation
 <222> (1)..(19)
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 b at position 4 = c or g or t; k at position 6 =
 g or t.

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21

<210> 8
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 <212> PRT
 <213> Homo sapiens

<220>
 <223> Amino acid sequence corresponding to the
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 11.

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 1 5

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 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

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 <221> variation
 <222> (8)..(27)
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 k at position 9 = g or t.

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29

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<211> 9
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Ser Trp Arg Cys Asp Cys Gly Leu Gly
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<210> 11
<211> 3586
<212> DNA
<213> Mus musculus

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<222> (1411)..(3108)
<223> Platelet glycoprotein V gene

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caattgccta aagttttctg acaccacaaa gtgaggcact gccacatgca cccacatact 180
cctgcacagg aatgagttag tgcaatgtag catggaaaaa aaccaaaagt gtggcccatg 240
taatgacagc ctgctatttc tgggaaaact taggcctct actctctagc ttttacaaaa 300
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gcagttagag gctcagtctg tataggggca gaaggagacc tggtaacaaga aacagtacaa 600
atttttactt gggaaacaga gtaaactagt attactgtgt gcttcctggg taactcaatg 660
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170

175

180

ctg ccc aag gga ctg ctt ggg gct caa gtt aag ctt gag aaa ctg ctg	2010
Leu Pro Lys Gly Leu Leu Gly Ala Gln Val Lys Leu Glu Lys Leu Leu	
185 190 195 200	
ctc tat tca aac cag ctc acg tct gtg gat tcg ggg ctg ctg agc aac	2058
Leu Tyr Ser Asn Gln Leu Thr Ser Val Asp Ser Gly Leu Leu Ser Asn	
205 210 215	
ctg ggc gcc ctg act gag ctg cgg ctg gag cgg aat cac ctc cgc tcc	2106
Leu Gly Ala Leu Thr Glu Leu Arg Leu Glu Arg Asn His Leu Arg Ser	
220 225 230	
gta gcc ccg ggt gcc ttc gac cgc ctc gga aac ctg agc tcc ttg act	2154
Val Ala Pro Gly Ala Phe Asp Arg Leu Gly Asn Leu Ser Ser Leu Thr	
235 240 245	
cta tcc gga aac ctc ctg gag tct ctg ccg ccc gcg ctc ttc ctt cac	2202
Leu Ser Gly Asn Leu Leu Glu Ser Leu Pro Pro Ala Leu Phe Leu His	
250 255 260	
gtg agc agc gtg tct cgg ctg act ctg ttc gag aac ccc ctg gag gag	2250
Val Ser Ser Val Ser Arg Leu Thr Leu Phe Glu Asn Pro Leu Glu Glu	
265 270 275 280	
ctc ccg gac gtg ttg ttc ggg gag atg gcc ggc ctg cgg gag ctg tgg	2298
Leu Pro Asp Val Leu Phe Gly Glu Met Ala Gly Leu Arg Glu Leu Trp	
285 290 295	
ctg aac ggc acc cac ctg agc acg ctg ecc gcc gct gcc ttc cgc aac	2346
Leu Asn Gly Thr His Leu Ser Thr Leu Pro Ala Ala Ala Phe Arg Asn	
300 305 310	
ctg agc ggc ttg cag acg ctg ggg ctg acg cgg aac ccg cgc ctg agc	2394
Leu Ser Gly Leu Gln Thr Leu Gly Leu Thr Arg Asn Pro Arg Leu Ser	
315 320 325	
gcg ctc ccg cgc ggc gtg ttc cag ggc cta cgg gag ctg cgc gtg ctc	2442
Ala Leu Pro Arg Gly Val Phe Gln Gly Leu Arg Glu Leu Arg Val Leu	
330 335 340	
gcg ctg cac acc aac gcc ctg gcg gag ctg cgg gac gac gcg ctg cgc	2490
Ala Leu His Thr Asn Ala Leu Ala Glu Leu Arg Asp Asp Ala Leu Arg	
345 350 355 360	
ggc ctc ggg cac ctg cgc cag gtg tcg ctg cgc cac aac cgg ctg cgg	2538
Gly Leu Gly His Leu Arg Gln Val Ser Leu Arg His Asn Arg Leu Arg	
365 370 375	
gcc ctg ccc cgc acg ctc ttc cgc aac ctc agc agc ctc gag agc gtg	2586
Ala Leu Pro Arg Thr Leu Phe Arg Asn Leu Ser Ser Leu Glu Ser Val	
380 385 390	
cag cta gag cac aac cag ctg gag acg ctg cca gga gac gtg ttc gcg	2634
Gln Leu Glu His Asn Gln Leu Glu Thr Leu Pro Gly Asp Val Phe Ala	

0975303-020504

395	400	405	
gct ctg ccc cag ctg acc cag gtc ctg ctg ggt cac aac ccc tgg ctc Ala Leu Pro Gln Leu Thr Gln Val Leu Leu Gly His Asn Pro Trp Leu 410 415 420			2682
tgc gac tgt ggc ctg tgg ccc ttc ctc cag tgg ctg cgg cat cac ccg Cys Asp Cys Gly Leu Trp Pro Phe Leu Gln Trp Leu Arg His His Pro 425 430 435 440			2730
gac atc ctg ggc cga gac gag ccc ccg cag tgc cgt ggc ccg gag cca Asp Ile Leu Gly Arg Asp Glu Pro Pro Gln Cys Arg Gly Pro Glu Pro 445 450 455			2778
cgc gcc agc ctg tcg ttc tgg gag ctg ctg cag ggt gac ccg tgg tgc Arg Ala Ser Leu Ser Phe Trp Glu Leu Leu Gln Gly Asp Pro Trp Cys 460 465 470			2826
ccg gat cct cgc agc ctg cct ctc gac cct cca acc gaa aat gct ctg Pro Asp Pro Arg Ser Leu Pro Leu Asp Pro Pro Thr Glu Asn Ala Leu 475 480 485			2874
gaa gcc ccg gtt ccg tcc tgg ctg cct aac agc tgg cag tcc cag acg Glu Ala Pro Val Pro Ser Trp Leu Pro Asn Ser Trp Gln Ser Gln Thr 490 495 500			2922
tgg gcc cag ctg gtg gcc agg ggt gaa agt ccc aat aac agg ctc tac Trp Ala Gln Leu Val Ala Arg Gly Glu Ser Pro Asn Asn Arg Leu Tyr 505 510 515 520			2970
tgg ggt ctt tat att ctg ctt cta gta gcc cag gcc atc ata gcc gcg Trp Gly Leu Tyr Ile Leu Leu Leu Val Ala Gln Ala Ile Ile Ala Ala 525 530 535			3018
ttc atc gtg ttt gcc atg att aaa atc ggc cag ctg ttt cga aca tta Phe Ile Val Phe Ala Met Ile Lys Ile Gly Gln Leu Phe Arg Thr Leu 540 545 550			3066
atc aga gag aag ctc ttg tta gag gca atg gga aaa tcg tgt Ile Arg Glu Lys Leu Leu Leu Glu Ala Met Gly Lys Ser Cys 555 560 565			3108
aactaatgaa actgaccaga gcattgtgga cggggcccca aggagaatgc agtcaggatg			3168
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<212> PRT

<213> Mus musculus

<400> 12

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35 40 45

Pro Thr Asn Leu Thr His Ile Leu Leu Phe Arg Met Asp Gln Gly Ile
50 55 60

Leu Arg Asn His Ser Phe Ser Gly Met Thr Val Leu Gln Arg Leu Met
65 70 75 80

Leu Ser Asp Ser His Ile Ser Ala Ile Asp Pro Gly Thr Phe Asn Asp
85 90 95

Leu Val Lys Leu Lys Thr Leu Arg Leu Thr Arg Asn Lys Ile Ser Arg
100 105 110

Leu Pro Arg Ala Ile Leu Asp Lys Met Val Leu Leu Glu Gln Leu Phe
115 120 125

Leu Asp His Asn Ala Leu Arg Asp Leu Asp Gln Asn Leu Phe Gln Gln
130 135 140

Leu Arg Asn Leu Gln Glu Leu Gly Leu Asn Gln Asn Gln Leu Ser Phe
145 150 155 160

Leu Pro Ala Asn Leu Phe Ser Ser Leu Arg Glu Leu Lys Leu Leu Asp
165 170 175

Leu Ser Arg Asn Asn Leu Thr His Leu Pro Lys Gly Leu Leu Gly Ala
180 185 190

Gln Val Lys Leu Glu Lys Leu Leu Leu Tyr Ser Asn Gln Leu Thr Ser
195 200 205

Val Asp Ser Gly Leu Leu Ser Asn Leu Gly Ala Leu Thr Glu Leu Arg
210 215 220

Leu Glu Arg Asn His Leu Arg Ser Val Ala Pro Gly Ala Phe Asp Arg
225 230 235 240

Leu Gly Asn Leu Ser Ser Leu Thr Leu Ser Gly Asn Leu Leu Glu Ser
245 250 255

Leu Pro Pro Ala Leu Phe Leu His Val Ser Ser Val Ser Arg Leu Thr
 260 265 270
 Leu Phe Glu Asn Pro Leu Glu Glu Leu Pro Asp Val Leu Phe Gly Glu
 275 280 285
 Met Ala Gly Leu Arg Glu Leu Trp Leu Asn Gly Thr His Leu Ser Thr
 290 295 300
 Leu Pro Ala Ala Ala Phe Arg Asn Leu Ser Gly Leu Gln Thr Leu Gly
 305 310 315 320
 Leu Thr Arg Asn Pro Arg Leu Ser Ala Leu Pro Arg Gly Val Phe Gln
 325 330 335
 Gly Leu Arg Glu Leu Arg Val Leu Ala Leu His Thr Asn Ala Leu Ala
 340 345 350
 Glu Leu Arg Asp Asp Ala Leu Arg Gly Leu Gly His Leu Arg Gln Val
 355 360 365
 Ser Leu Arg His Asn Arg Leu Arg Ala Leu Pro Arg Thr Leu Phe Arg
 370 375 380
 Asn Leu Ser Ser Leu Glu Ser Val Gln Leu Glu His Asn Gln Leu Glu
 385 390 395 400
 Thr Leu Pro Gly Asp Val Phe Ala Ala Leu Pro Gln Leu Thr Gln Val
 405 410 415
 Leu Leu Gly His Asn Pro Trp Leu Cys Asp Cys Gly Leu Trp Pro Phe
 420 425 430
 Leu Gln Trp Leu Arg His His Pro Asp Ile Leu Gly Arg Asp Glu Pro
 435 440 445
 Pro Gln Cys Arg Gly Pro Glu Pro Arg Ala Ser Leu Ser Phe Trp Glu
 450 455 460
 Leu Leu Gln Gly Asp Pro Trp Cys Pro Asp Pro Arg Ser Leu Pro Leu
 465 470 475 480
 Asp Pro Pro Thr Glu Asn Ala Leu Glu Ala Pro Val Pro Ser Trp Leu
 485 490 495
 Pro Asn Ser Trp Gln Ser Gln Thr Trp Ala Gln Leu Val Ala Arg Gly
 500 505 510
 Glu Ser Pro Asn Asn Arg Leu Tyr Trp Gly Leu Tyr Ile Leu Leu Leu
 515 520 525
 Val Ala Gln Ala Ile Ile Ala Ala Phe Ile Val Phe Ala Met Ile Lys
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 Ile Gly Gln Leu Phe Arg Thr Leu Ile Arg Glu Lys Leu Leu Leu Glu
 545 550 555 560

Ala Met Gly Lys Ser Cys
565

<210> 13
<211> 7452
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (2422) .. (4101)
<223> Platelet glycoprotein V gene

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gcattaggct gcatcaaagg ggattggatc ccatgattct ttatatcttc tgacattaag 180
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Leu Gly Leu Leu Arg Ala Gln Pro Phe Pro Cys Pro Pro Ala Cys Lys
15 20 25
tgt gtc ttc cgg gac gcc gcg cag tgc tcg ggg ggc gac gtg gcg cgc 2547
Cys Val Phe Arg Asp Ala Ala Gln Cys Ser Gly Gly Asp Val Ala Arg
30 35 40
atc tcc gcg ctg ggc ctg ccc acc aac ctc acg cac atc ctg ctc ttc 2595
Ile Ser Ala Leu Gly Leu Pro Thr Asn Leu Thr His Ile Leu Leu Phe
45 50 55

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Gly Met Gly Arg Gly Val Leu Gln Ser Gln Ser Phe Ser Gly Met Thr	
60 65 70	
gtc ctg cag cgc ctc atg atc tcc gac agc cac att tcc gcc gtt gcc	2691
Val Leu Gln Arg Leu Met Ile Ser Asp Ser His Ile Ser Ala Val Ala	
75 80 85 90	
ccc ggc acc ttc agt gac ctg ata aaa ctg aaa acc ctg agg ctg tcg	2739
Pro Gly Thr Phe Ser Asp Leu Ile Lys Leu Lys Thr Leu Arg Leu Ser	
95 100 105	
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Arg Asn Lys Ile Thr His Leu Pro Gly Ala Leu Leu Asp Lys Met Val	
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Leu Leu Glu Gln Leu Phe Leu Asp His Asn Ala Leu Arg Gly Ile Asp	
125 130 135	
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Gln Asn Met Phe Gln Lys Leu Val Asn Leu Gln Glu Leu Ala Leu Asn	
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Gln Asn Gln Leu Asp Phe Leu Pro Ala Ser Leu Phe Thr Asn Leu Glu	
155 160 165 170	
aac ctg aag ttg ttg gat tta tcg gga aac aac ctg acc cac ctg ccc	2979
Asn Leu Lys Leu Leu Asp Leu Ser Gly Asn Asn Leu Thr His Leu Pro	
175 180 185	
aag ggg ttg ctt gga gca cag gct aag ctc gag aga ctt ctg ctc cac	3027
Lys Gly Leu Leu Gly Ala Gln Ala Lys Leu Glu Arg Leu Leu Leu His	
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Ser Asn Arg Leu Val Ser Leu Asp Ser Gly Leu Leu Asn Ser Leu Gly	
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Pro Gly Ala Phe Asp Arg Leu Pro Asn Leu Ser Ser Leu Thr Leu Ser	
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Arg Asn His Leu Ala Phe Leu Pro Ser Ala Leu Phe Leu His Ser His	
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Asn Leu Thr Leu Leu Thr Leu Phe Glu Asn Pro Leu Ala Glu Leu Pro	
270 275 280	

00500-00000

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Gly	Val	Leu	Phe	Gly	Glu	Met	Gly	Gly	Leu	Gln	Glu	Leu	Trp	Leu	Asn	
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Arg	Thr	Gln	Leu	Arg	Thr	Leu	Pro	Ala	Ala	Ala	Phe	Arg	Asn	Leu	Ser	
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cgc	ctg	cgg	tac	tta	ggg	gtg	act	ctg	agc	ccg	cgg	ctg	agc	gcg	ctt	3411
Arg	Leu	Arg	Tyr	Leu	Gly	Val	Thr	Leu	Ser	Pro	Arg	Leu	Ser	Ala	Leu	
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Pro	Gln	Gly	Ala	Phe	Gln	Gly	Leu	Gly	Glu	Leu	Gln	Val	Leu	Ala	Leu	
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His	Ser	Asn	Gly	Leu	Thr	Ala	Leu	Pro	Asp	Gly	Leu	Leu	Arg	Gly	Leu	
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 Phe His Arg Asn His Ile Arg Ser Ile Ala Pro Gly Ala Phe Asp Arg
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 Met Gly Gly Leu Gln Glu Leu Trp Leu Asn Arg Thr Gln Leu Arg Thr
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 Leu Pro Ala Ala Ala Phe Arg Asn Leu Ser Arg Leu Arg Tyr Leu Gly
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 Ser Leu Arg Arg Asn Arg Leu Arg Ala Leu Pro Arg Ala Leu Phe Arg
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 Asn Leu Ser Ser Leu Glu Ser Val Gln Leu Asp His Asn Gln Leu Glu
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 Leu Pro Gly Gly Asp Ala Glu Cys Pro Gly Pro Arg Gly Pro Pro Pro
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Ala Pro Asn Ser Ser Glu Pro Trp Val Trp Ala Gln Pro Val Thr Thr
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Gly Lys Gly Gln Asp His Ser Pro Phe Trp Gly Phe Tyr Phe Leu Leu
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Lys Ile Gly Gln Leu Phe Arg Lys Leu Ile Arg Glu Arg Ala Leu Gly
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